Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

Please cancel claims 1-46 without prejudice and add new claims 47-64 as follows:

47. (New) A method for identifying a potential modulator compound for ErbB2 which method comprises:

(a) designing or selecting a compound which binds to the structure formed by amino acids 1 to 509 of an ErbB2 polypeptide having the atomic coordinates shown in Appendix I, or atomic coordinates having a root mean square deviation of backbone atoms of not more than 1.5Å when superimposed on the corresponding backbone atoms having the atomic coordinates shown in Appendix I, wherein binding of the compound to the structure is favoured energetically; and

(b) testing the compound designed or selected in (a) for its ability to interact with and/or modulate the activity of ErbB2.

48. (New) A method as claimed in claim 47, wherein the compound binds to a subset of amino acids selected from at least one of the CR1 domain, the potential CR1 loop docking site between the L1, CR1 and L2 domains, the CR1-L2 hinge region, the regions of the L1 and L2 domains that contact each other in a closed conformation.

49. (New) A method as claimed in claim 47, wherein the subset of amino acids defines at least a part of the heterodimerisation surface with another member of the EGF receptor family.

50. (New) A method as claimed in claim 49, wherein the member of the EGF receptor family is selected from the group consisting of ErbB1 (EGF receptor), ErbB3 and ErbB4.

51. (New) A method as claimed in claim 49, wherein the heterodimerisation surface includes at least one of (i) the N-terminal end of the CR1 domain, (ii) the CR1 domain dimerisation loop and adjacent residues and (iii) the C-terminal end of the CR1 domain.

52. (New) A method according to claim 51, wherein the surface comprises at least one of residues selected from 200-203, 210-213, 216-218, 225-230, 247-268, 244-246, 285-289) and 294-319.

53. (New) A method as claimed in claim 48, wherein the subset defines the CR1 loop docking site.

54. (New) A method as claimed in claim 53, wherein the docking site comprises at least one of the following ErbB2 residues: Gln 36, Gln 60, Arg 82, Thr 84, Gln 85, Phe 237, Thr 269, Phe 270, Gly 271, Ala 272, Tyr 282, Thr 285, Gly 288, Ser 289, Cys 290, Thr 291, Leu 292, Val 293, Cys 294, Pro 295 and Cys 310.

55. (New) A method as claimed in claim 47 wherein the method is performed *in silico*.

56. (New) A method as claimed in claim 55, wherein the candidate compound is selected from a real compound, a virtual compound or a combination thereof.

57. (New) A method as claimed in claim 56, wherein the compound is in a library with at least one other candidate compound.

58. (New) A method as claimed in claim 56, wherein the method is used for targeted screening.

59. (New) A method as claimed in claim 57, wherein the library comprises an array of maximally diverse compounds.

60. (New) A crystal of ErbB2 polypeptide.

61. (New) A crystal of ErbB2 polypeptide having a space group $P2_12_12_1$ with unit cell dimensions of a=75.96 Å, b=82.24 Å, and c=110.06 Å, with up to about 1% variation in any cell dimension

62. (New) A crystalline composition comprising a crystal of ErbB2.

63. (New) An antibody that binds to ErbB2, the antibody being directed against at least one of the N-terminal end of the CR1 domain, the CR1 domain dimerisation loop and adjacent residues and the C-terminal end of the CR1 domain.

64. (New) An antibody as claimed in claim 63, the antibody being directed against a structure defined by (i) ErbB2 amino acid residues 200-203, (ii) ErbB2 amino acid residues 210-213, (iii) ErbB2 amino acid residues 216-218, (iv) ErbB2 amino acid residues 225-230, (v) ErbB2 amino acid residues 247-268 or a subset thereof; (vi) ErbB2 amino acid residues 244-246, (vii) ErbB2 amino acid residues 285-289, or (viii) ErbB2 amino acid residues 294-319 or a subset thereof.